

Sequence listings

SEQ ID NO: 1

Homo sapiens transforming growth factor, beta receptor II (70/80kDa),
complete antisense sequence

Derived from AY675319

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1 CAGCCACACT GTCTTTAACT CTCAGCCCAC CCACACTGAG GAGGGTGCCT AGAGGTTCTA
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29101	CTTTGGAAGA	CAGAAAAAAA	AAGAATTTGA	CATTTGTCTT	TAAAAAATA	TTTATGTAAC
29161	AAGACTCTGA	CATTTGCAAA	TGGCTCCTTA	TTTGCAACTA	AGTCTGGCCT	CTATGAGTGA
29221	CAGAAGTGAC	TGGAATTTT	CAGAATTATT	AAATGGATCT	CACAGTTCAT	TGTTAAGGAG
29281	ATAGCTTGGT	GGTATGGAAA	GAACAAAAGC	TTTGAAGCCA	CTCAGATGAT	TAAAAAATA
29341	TGGGGGGAAG	ATATGGTGCC	TCACACCTGT	AATCCCAGCA	CTTCGTGAGG	CTGAGGTGGG
29401	AGGATCACTT	GAGCCCAGGA	GTTTGACACC	AGCCTGGGCA	ATATATTGAG	ACCCTGTCTG
29461	TATAAAAAAA	AAAAAAATT	AGCTGGATGT	GGTGGTGTGG	GCATGTAATC	TGAGCTACTT
29521	AAAAGGCTGA	GGCAGGAGGA	TCACGAGCCC	AGAAGTTCAA	GACTGCAGTG	AGCTATAATG
29581	GTGCCACTGC	ATTTTAGCCT	GGGCAACAGA	ACGAGAACAT	CTCCCCCTGC	CCCCCAACT
29641	CCCCCCCCCA	AAAAAGTTAG	CCCTCTCTTC	CTCTTTCTTT	TCTCCTAAGG	GTATTTAAAA
29701	TAATATACTT	GGCCCAAGAG	CACAGTATGG	CCCTCAAAAC	TAGAGAAATT	ACTCTGATTT
29761	CTCTCTTGTG	AAAAAGAATT	CATTCCAAAA	TAAAACACAG	ATACAGAAAA	GTGCATAAAA
29821	CAAGTGTCTG	GCTTAGTGAA	TTACTATAAG	ATCAACACTC	TTGTAACCAC	TGGTCAGGTC
29881	AGAAAATATA	ATTTTGCTGG	CCACCCCAGA	AGTCTGTTCA	TGTTCCCCAA	CTCAATCGGA
29941	GATCCCTCCC	TTCTCTAAA	AAGTAATCAC	TATTCCTGGC	TTTTATAGTT	ATCATTTTCT
30001	TGAGCTTTTA	AACTTGTTTT	ATCATCCAAG	TATGCATCTG	TAGTCGTCTT	GCTACTAATA
30061	TGACTGAATA	CAAATGGCAA	ACCTTGCTTT	TTTGCAAGAT	TACTGTTTTA	AAAAAATTCT
30121	CTACAATAAA	AACACCAGAA	TCTTTAAAAA	ATGTTTAATC	TGAATTAATC	AAATCATCAG
30181	ACAAATCTAC	AAAGTGCCCT	TATAAAGTAC	ATGAAATGGT	CTGACCTATT	CAAATCAAAG
30241	TCAATGTCAT	GAAAACCAAA	AAAACACACT	GTAGAGGCAA	AACAATCAAT	TTTAATGTGT
30301	TGTCCTTGAC	TGGATTCCGA	ATTTAAACAA	TAGACCCATT	AACCTTGAAG	AAATCTGAAT
30361	ATGGACTGTA	CTGTATATAT	ATTTAGATGT	ATATATGTGA	ATGTATCTGT	GTCTTAGTAT
30421	CTGTATACAC	ACACACACAC	ACAGAAAGAG	AGTGAAAGCT	AAGCACTCAC	ATATATGCTT
30481	CATATTGCAG	AGTTCAAAGA	TCTTGCCATC	ATTTTCTGTA	CCTTTAAAAA	TTTTGTTGGC
30541	ATGTTACATA	AAGAATAACT	TGTCACCTCG	TTATTCTAAG	TGTGCCCCGA	GACCAGCAGT
30601	CATCAGCATC	CCCTGGGAAC	TTACTGGAAA	TGCAGAGTCT	TAGCGCTGTC	CTCAACTAAC
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30721	AGGTAAATTT	TATTCTTGCT	AAACAGTTTA	GCAAAAATAA	AGTTAAGTTC	TTTGGTACTC
30781	TGCCATAGAG	ATGCTTTCCT	CCTACAAAAA	ATTTCTTAGT	GGAATTGTTT	GCAAAGCTCT
30841	GGTACAGCTG	TATTCAGCAC	TAGCCAATGA	GAAAATGGCC	CATGATAATT	TTCTAGTCAA
30901	TTAACTGGTG	GAGGAGTGTA	GAATGAGATA	TGCTTCCCCA	TCCATCATCC	TAGTAAAAAG
30961	CACACCAATT	TAGGCAAACA	ATAAAAAGTC	ATTTCAATTA	AACAACAAAA	GGACAGTAAG
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31081	TGGATATATT	TTGAGAGTAT	TTTTTCCTCA	AATGATGAAA	GAAGTCTTCT	CTCCAATCAA
31141	TGTGGTTGTT	TTATTCCAAC	TGCACATATT	TCAGAACAAA	GCTATTTCGCC	ACCTCTCCTA

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31321	GTGAAACCTC	TGCCTGAAAA	TGTTATGGTA	GAAGGACATC	ATTCCTTTGT	TATCATTCCA
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31441	ATGTTTAAAA	TTATTCTTTA	CATTAAGTCA	AATGTAGCCT	CTGTGTGCTT	CTATTATTGG
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31561	AACTATTAAA	CTCCTGCTGG	ATATGAAACT	CACAACCCCT	AGATCATTTT	ATTTTCAGGT
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31741	GGACCTTTTT	TCTAAGGGTA	AAGTGATCTG	TTCTCTGAAA	CCACGCTTGC	TATTTAAGAT
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32161	TAGGCATCCC	TTCCACTGTG	CTTTTCACCC	TTTATGTTCC	TCCTTAGGAT	ATAGATTCCCT
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32521	TCTCAGGAAA	CCTGAAAGCA	AGGTACATTT	CTTAAGTTAT	TTCAGGATGC	TCTCCAACAG
32581	GGAGACCAGA	TCGCTTTGGA	AAAGCATATT	CATTATTAC	AATACCTGTT	AGGTACACAG
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32701	CCACCTGAGT	TTCTCACCTC	CTAAAATCAT	GCACACAGCC	TCCCTGGTCC	CTGCCTTGTC
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32881	AATGAGGCCG	TTGACCTTGT	TCCAAAGCAA	TTGCTTGTA	ATTGTTGTAG	AAAACAAAAT
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33601	CGATTTAGAA	TACAAAAGGA	CTTTCCAAAG	GCAAGTCATC	CAGATGTCCA	AATGGTGGTG
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33721	CCTCCCTGAG	CCTTTTTTTT	CCCCTGGTGG	GACACTGAGA	CACTCGCAAA	GCAGCAAAAG
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72001	TCCAATAAGT	GCCACAGAAT	ATTAAGACTT	AAGAATATTA	AAATTCTGGT	CAGGTGCAGT
72061	GGCCCATGCC	TGTAATCCCA	GCACTTTGGG	AAGCCGAGGA	GGGTGGATTG	CCTGAGGTCA
72121	GAAGTTCAAG	AGCAGCATGG	CCAACATGGC	AAAACCCTGT	CTCTACTAAA	AATACAAAAA
72181	TTAGCCAGGT	GTGGTAGTGG	GCACCTACAA	TCCCAGCTAC	TCGGGAGGCT	GAGGCAGGAG
72241	AATAACTTGA	ACCCAGGAGG	CAGAGGTTGC	AGTGAGCTGA	GGTCGTGCCA	TTGTACTCCA
72301	GCCTGGGTGA	GAAGAACAAA	ACTCTGTCTC	AAAAAAAAAA	AAAAAAAAAG	AATATTAAAA
72361	TTCTTATTTT	ATCTCCTTTT	CCTCTATAGA	TAGAGCAGGT	AGGGCACTAC	CAGTCCAAAT
72421	CTATGTAATG	TGATGTCAGT	GGTAGCTCCA	GAATTCCCAT	AGAGGAGTGG	CTACATGGGT
72481	GATGATCTGG	CTGAAAGGGA	GGCAGGCAAC	ACAGCTGGAA	GCTGTGCTTG	CACAAGAGAA
72541	CACTACTTGT	GGTACCTAGA	CTGCATGTTT	ATTCAGGATG	GATGGGGACT	ATGGTGGACG
72601	AGAAGGCTGA	AGGCCAAATT	CAAGACCATC	CTTAGAAACC	CACTCCTATT	AAGCACCCAG
72661	GTAAGAAAGG	CCTCATATTT	AAGTCTCCTT	AGCATGTATC	ATTTTAACAG	GGCTTTCCAA
72721	AAAGTACAAC	CAGGGGTCAC	CTTTGCAATA	TGGGATTATT	TACCCTCAGG	TAGGTAGAAG
72781	AGTATCTTCA	GCCACTCTTC	ATTGCACCAA	GACCCCTTCA	GCCATCCCTA	TTCCAGCAAT
72841	CCCAATGACT	GAAATCATCT	ATGACTCATA	AAGAGAAAAA	GCAGGAGTGA	CAAAAAATTG
72901	TCCTGCGTGA	GATGGTGTGA	TTTACTTTAT	GACTTTGCCT	GGTCTCTATA	GTCATAATGC
72961	ATTGAGCCTT	CTGCAAAAGA	TTCACACATG	AGAGAATAAA	TGAATCAAAG	GCAGAGCCAG
73021	TGATGGATGG	AAAATTAACC	TTAACACCCA	CACACCACAG	CTCCCCAAAA	TTCACAGAAA
73081	CTAAAGACTG	CAGACAGAGC	AAGTCTCCAC	TGTAAAGAAC	AATTTACACA	AAGCAGATCA
73141	TACGAGATTT	TCCATAAGCC	TATGGTTCTG	TCAAACAATA	CTACAGGTGG	CTTTAAGCCA
73201	TTGACATTTA	CAC'TTGGTGG	TGAAAAGCCA	TCTGGGAGAA	AAAAAAATAG	CACTCCCCGC
73261	CTTGGATCTA	AAAGCAAGTT	TCCTCGGCCT	TTAAAAGCAA	TGAATTCCAA	ACAGCAACAA
73321	ACAAAACACA	TAAACAGAAT	TAGTGAGAAT	CTGTGCTAAG	AGCTATGGCA	AAATCAGACA
73381	GAAGTTTCTC	CCTCAAAGAG	TTTTTATTCT	AGTAAGAGTT	TTGTTTTGTT	TTGTTTGT

73441	TGAGACAGAG	TCTCACTCTG	TCGCCTAGGC	TGGAGTGCAG	TGGCGCGATC	TCGGCTCACT
73501	GCAAACCTCCG	CCTCCCAGGT	TCACGCCATT	CTCCTGCCTC	AGCCTCCCCG	GTAGCTGGGA
73561	CTACAGGCAC	CCGCCACCAC	GCCCAGCTAA	TTTTTTGTAC	TTTTAGTAGA	GACAGGGTTT
73621	CATCGTGTTA	GCGAGGATGG	TCTCGATCTC	CTGACTTCGT	GATCCGCCCC	CCTCGGCCTC
73681	CCAAAGTGCT	GGGATTACAG	GCATAAGCCA	CCACGCCTGG	CTAGTAAAAT	AGTTTAA AAC
73741	ACACAGAGAC	AGCACAGGTA	GCTTGGCAAA	CAAGGTCATA	TGAATGAGAA	TGCAAGGCTT
73801	GTCGGAGAGG	CTATGGGCAG	GAAAAGGAAT	CACAGTGGGA	TGGATAATCA	AGGAAGGCCC
73861	ACTAGAAAAA	GTAACATTTA	GACCAGGCGT	TATTTCAAAG	GGTGGAGCCG	TTGTAGGGCA
73921	CAAATAGAGA	ATGGTAA AAC	TTGGGGGGAG	GTGGTGGAGA	ATGGTCACAA	GCTAGGAAAT
73981	TTGTAAGCAA	AAAGGATGTG	TGAGGCAGCT	GGGTTCAAGT	GGAACCAGGG	CATGAGGGAT
74041	GTGAAGGGTG	GAATAGATGA	TGGGCAAGAG	GTTTGGCTTC	ATCTGTGCAC	GTAGTCATCA
74101	AACTGGTCCT	GTGTCCCATC	AGCACAAGGC	ACTCTCTTAG	GAGCCAAGGG	AACTGAGGC
74161	AGCCCCCATG	CTCAAAGAGA	AAGGGAAGGC	CATGTGATGA	TCTAGGATTC	ATAAAATCCA
74221	TGGAAGGCTT	TCTAACAGAG	GCCAGCTATT	CAAAATGCCA	TCTGGGGGGA	GATTTAACTG
74281	AGGGCAATGC	CTGTGTTATT	GACAGAGAAA	GAACAAAGGG	TGTCCATAAG	CAGAGACCAA
74341	TTAGGTGATT	TTTACAGATG	ACAAATATAA	GAGTTCAGGT	TTGTGTTACG	GTAGCATAAT
74401	TCAAGGGCAA	AAATAAAACC	AAATGGTTAT	AGATTTTGCG	TAACTTTCT	GATGGATAAC
74461	TTAAGATTTG	ATGCAACAGG	AATCACCATG	AGATATGAGT	TGCAATGGAA	AGTTTTTATG
74521	TTTTTTTTTTC	TTGCCAAGTA	TAGTTCAGAT	GTCAAAGGCA	AAGAAAAAAA	AGTCAGAAAA
74581	TAAAATTATT	TGGAAACATC	AGAACTGCT	TGTAAGGACT	GTTATTGTG	GCTACTGTTA
74641	ATTAAGAGCA	TTAATAACTG	ACAGGGACCC	ATAATTCTGG	AAGACAAAAG	TAATAAGTC
74701	ACAAAAAGCT	GCCTTATGAT	ATTAAAATAA	AGGAGCAAAT	CAATGAAAAA	GCCTACAGTG
74761	GCACTCTCAG	AAAAGTCTAA	AACAAATGTT	GAGCAATTCA	AGAGAAATTT	ATTGGGTCTT
74821	CACTGAGCAT	CAGACAAATA	AGTTCCTCAA	GACAAAAGAG	GATTAATAAA	TGTTGAAGAG
74881	TAAAACCACT	TCCTGAAAAC	CTGTCATCGA	ATCATTAATT	TATTGGGTAC	CTACTTTGTA
74941	TAGAGCAGAG	TGCTACCTAT	TTTAAGAAAT	GCTGTGGTAT	AATAGCTCCA	GAATGAATTA
75001	GGGCCTACAT	ATGTCAAGGC	AATCTGTGAG	TAAATGCCTA	ATGAGGTAAA	CATGATTAAT
75061	GCAGTGAGTT	CGATATAGAA	ATGGGTCCTT	GGGGCCGGAC	ACGATGGCTC	GTGCCTGTAA
75121	TCCCAGCACT	TTGGGAGGCC	GAGGCGGGCG	GATCACGAGG	TCAGGAGTTT	GAGACCAGCC
75181	TGACCAACAT	GGTGAAACCG	TGTCTCTACT	AAAAATACAA	CAACAACAAA	ATTAGTCAAG
75241	TGTGTTGGTG	CACACCTGTA	ATCCCAGCTA	CTCAGGAGGC	TGAAGCAGGA	GAATCGCTTG
75301	AACCCAGGAG	GCAGAGGTTG	CAGCGAGCCG	AGATTGCGCC	ACTGTACACC	AGCCTGGGCA
75361	ACAGAGCGAG	ATTCCATCTC	AAAAAAAAAA	AAAAACAAG	AAAGAAAAAA	GAAATGGGTC
75421	CTTGGGTTCT	ACAGTTCACC	ATGGTCAAGG	GATGGACAAT	CAGTGGACAA	AAGACTCATG
75481	AAGGATGACT	GGGGAACAG	ACTGGTTAAA	AACTGACTCA	TTTAGTTGAC	TTGCTACCAG
75541	TGCCTTCTGT	CTTCTGCTAG	CTTTAGTTAA	AACGGCTTAG	GAAGAGTCAA	AAGACTCTCA
75601	TAAAACTAAG	CCAACCTTTC	CTTGAATTCT	CCTCTTCTTT	ATTGACAGAA	ACAAGCCTGA
75661	TGTGATCCAC	TAAAACCACT	GCAGATCATT	TGGCTACTCT	TTGGAACATG	CTTTAATGCT
75721	ATTACAGCAG	TGTTTTTCAA	ACTGCTATGT	GTACAGGAAT	CACCTGGGGA	CCTTGTGAAA
75781	GTGTACATTC	TGTTGCAGTA	GGTCTGGGGA	GAGGACCCAC	AATCCTCATT	TCCAATAAAT
75841	TCTCAGTGAT	GCCAGACCTC	CTGTAAGCGG	CAAGGTATTA	GAACATCTTC	AGTTGCTGTT
75901	ATCAGAAAGAT	GATAGGAAAC	CATCATTTTC	GGGGTCAGAA	TGCTGGAGCT	CAAGCTTTGG
75961	GCCTTGATGC	ATATAATAAC	TCATAAAATG	TAATATTCAG	GAAGGAATGA	GGCTCCTAAA
76021	GAAGTGAGAA	AGTAGAATGA	ACAAAGGCCT	AAGAGAATAG	AAATGTATTC	TAACAATATA

76081 AATTATAAAA ATAAAAGTAA GAGTGCCAG GGGTATTGAG ATTGTTAGAT TATTTTATAA
76141 TGATATAACT TAAGGGATTC CAAAATAATG AACATAAAAT GTTATTATTA GATTTTTTTC
76201 CTTTTCACAT ACTTGAAGGA CAAATTATAT CATATTGTCT TTTTTTCTTC CCCAATACTA
76261 TGAGCGTTAG AGAATGAGAC GCAAATCCGA TATGTAGTAA CAAGGTAGTC ACTCACAGCA
76321 AAAGTTGAAA GATTCCTAGT CTACGCTAAC AAGTGTCTGC AAACCTCTACA GAAATGCAAT
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76441 GCAAATTCTG TCTTTTCTGA GAATATTTTA AGAAAAGTGG TAGAGAAATA TTTGAAAGGC
76501 AACAGAACAC TAATTATATC TAGACAAGTT TCCTTTTTTT TTTTCCCAA AAAATATGAA
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76621 GGAAAAATTT TCACAGACAT TTTAACCAAT TCAGAGGAAG GGGAGAATGA AAATACCATA
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76741 GTGAGCTCTA GCTGAAGTAA ACATGCTATT TAGTCAGGAT GTATGCTCAG ACACCTGTAG
76801 TCGGAAATTT TCAAAATAGC TATGGTTTTT TTTCTTCTCT TTTTTTAATA GTAGTCATCT
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76921 TAGTTTTCTA TTTTGATTAG CTAAAGATTT TCTAACTCAA CTTCAATGAT TTATTCTACT
76981 AACAAAATAG TACAGGGATA ACAAAGAATG AAATGTTTCA GAAGAGAAAA TACTGGAAAT
77041 CTTATTTAGT CCAATTCTTG TCACTGTATA GAAGGAAAAT GAGCCCCAGT GGGAAGAAAG
77101 ACAGCCTGGT CACCCAGACA CCTAGATTCC TGGTACAACA TACCTTAGTC TTTACCAGCT
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77341 GTGAAATAAC AATGCAGATT TCAGTCTCTG TTTGCAATGG GGGGAAGGAG GAAGAGGCAT
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77821 TGATTATGCA ACTGCTTTCC AGACTGAGTG ACAGAATGAG ATCTCATCTC TGGAAAAAAA
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78721 CTTCCAACAC CCATGCTATA ATGGACAAGT AGTTTATGTC AATTAAGGCA GACTAGTCTC
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78841 AGCCTAATCA TTTTCTAACT AGGTGGACTT AGGCAAATTT ATTGACTCTG GAGGATTTAT
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78961 TCAGCATGAT CCGTGCAGTA GCAAGACCTC AATAAGTGGT AGCTACTATG ATTATTGGGA
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81481	TCTCCCTGAG	ATGAGACAAT	TTGCCTGTCC	AGCATTCCAA	ACCCTTTGGC	ATGCCAAGCA
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81601	ATTACCAGGA	AAGTAGAGAG	TGCAAAAGAA	GCGGTGAGCA	TTCTTGCTGC	GAATGCATAT
81661	CTGTTCTACT	GAAAATCATA	ACTTAAATCT	GCTGAAGTTG	TACATAAGGA	CCTGGAGGGT
81721	AGAAGCTAAC	AAGGTAACAG	AGTTATGCTT	TTATGTGGAA	CTTGGCCAAA	TAATGCCATG
81781	CTGTAGCCAG	GAAGTATGTT	TCCCCTGCAC	CCTATTTAAA	ACTGCTTTGG	TGGTTTGCAT
81841	CAGACCTAAA	TAATATCCAC	GCTACTCTAG	AGTAGGCAGT	GGTGGCTACA	AGACCACACT
81901	TCCCTTCAAC	CAACGCTGCT	TCACCCTTAT	AAACCAAAAC	ATAAAACCCA	ATGAAAAAAG
81961	AAACTTAAAA	AATAAATTTA	GATTTTAGCA	CTTCATTTCG	AATAAAATTC	TCTTTCCGAC
82021	ACCCTTCTAT	GAAAAAAAAA	AAAAAGAGGA	ATCAGTATCT	ACTGGATAAT	TCCTCTGGTG
82081	ACTTTATTTA	AAATTTTGCA	GTGGCTTTCA	AGGCCCTACA	CTGATTCAAA	ATTTATGGCT
82141	AAAGGAATTG	CATGAAAAC	TCTAGCAGCT	TTCCATCATG	TTTGTGAGAA	GTTGAAACAT
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82261	ACTTATTGTG	ATCAGAACTA	AACTATTCT	AACTGAAAGT	AAAGATTTTA	CTATTTGGAC
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82561	TCTGTATCTC	ATAGGAGACA	TTTACCTCAA	ACTGGGACAT	TCAAAGCAGG	TTTCTCAAG
82621	AAGATGACAC	TTGAACTACG	TCTTAAAAGA	TGAGTGAAAA	TTAGCCAGGT	AGCAGGAGTT
82681	CCAGACATCC	TGAACAAAGG	AACAGCTGCC	TAAATTGCTC	ACATTGTGTG	TATGTGTAGT
82741	GACACAAATA	GACTGGGAAA	ATGTGGGCTG	TGGTGGGATG	TGAAGCAGCA	GAGTCAAATG
82801	GGAACCAGGT	CAGAGGCCCC	TGGTAAGCCC	AATTAAGGAG	TTAATAGTAA	TAACAGAAGC
82861	TGATATTTAT	TGAGCATTTA	CTATGTTGCA	GGCACCATGT	TAAATACTTT	AAAACAATAT
82921	TTTATTTAAT	CCTCACCATA	ACTCCATAAT	CCTCATTTTA	CAAATGAGAC	CAGGGATGAC
82981	TAGTAGGTAA	AGCAACTACA	ACAGGCTACA	CAGCCAGTAC	ATGGCAAGTG	GGTCTGGAAC
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83101	AAGAGAGCAC	TAAATGAACG	CATTGGGTCC	ATCATGCTGG	CTATGGAATG	GAGAATGCAA
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83281	TGCATACAAC	AACAAAAAAA	AATGAGGCTT	TTGAAAATGA	GGTGTAGAAA	ATAAAACACC
83341	AGTATTCCAT	AATGCTTTCA	AATATAAACA	GTAAAAACAC	GTATCCTTTT	CTTTACTTAT
83401	AACATGCTCC	CAGCTGTTAA	ATTCAATGGC	AAAGACCAGG	TCTGTCTTAT	TCATCTGAGA
83461	TGGTATCCCA	GGTCTGAGCA	TCCTGCCTGG	CAAGAGATAC	TCAATAAATA	TGGTTGAAAA
83521	GGTAGAAGAA	AAAATGCCCA	GTTTTTGCAA	TGATATCAGA	GGTGCCTTAT	TGATCCAGAG
83581	TTAAAACTA	ACCTTACTGA	AAAAATTAAA	AAGTCATGTT	CATAACTGAG	TAGAAAACAT
83641	GTAGTAGTTA	TGTTGACTAC	ATAGACAACA	GTCATCATTA	GGGAATGCTA	CATTGAAAAG
83701	AAGGCAATGA	GTTCAAAAATG	TGATTAGTAT	TTTGTATAAA	TCATAACTCA	TTAAAAATAA
83761	GATGTTGAGT	GGCCTAAAGG	TGGAAATGTG	TTTTTATGAG	GCGGAAAAAA	AGCACGAGTA
83821	GACTGAAGAT	CAGATTTGGG	GCCTAATGAT	GTCTAGTCTC	TTACCCTGAC	AAAATAAGCA
83881	GGTTATTAAA	GTGATGTGAA	GAACCTGATC	ACTATGACAC	TTTTACAAAT	TCTTTGTCCT
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84061	GAGTGAATCT	ATTAAGTCAA	AAACGAAGAA	AAAAAACTT	TCTATTTCTT	AGTGAAATTT
84121	GTTCTTTTAT	TTAAATCCTT	TGCATACTAC	TAAACAGAAG	TACAGAAGCT	ACTAAACAGA
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84241	TCATTACCTG	ATATATTATC	TTGCATTAAG	ATATTTTGAA	AAAATGTTTT	CAGTTTACCA
84301	ATTACGTTAG	AGAAATTCTG	AAACTATTTA	CTTACATGAA	AAATTAAAAT	GTAAGTAGAA
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84601	GTGAACTATT	GGGTCTGGAA	TTTGCAAATC	ATAAACCTTA	TCCTTGTAAG	CAGAACCTAA
84661	CTAACAACAT	CAGGGCCTGC	TAATTTTCTT	CTTTTATAAT	CTGGAACAAA	AGTTGTAATG
84721	ATTTTTAACA	TCCACAGAAA	ATTAAGGGTG	CCATTTTAAA	TATTTATTAG	CAAAATGTCA
84781	CTTAGGTTTT	AAAAGTCTGG	AGGAAAATGA	GAGACAATTG	AACATTCTGG	TACTGCAATG
84841	CAGGAAAAAC	GCCAAGAACG	AAACACTAAG	ATTTTATTAA	AACCATAGGA	CTCAAATGTG
84901	TGTCAAGACT	TTTTGCTTGC	AATAGTGCCT	CTTCCTAATT	TGATTAAAAG	CTTCCATCTC
84961	CATGCCACCT	TCAATGTATG	CCATAATTTT	TAAAAAGTTC	CCAATCCACT	TCAAACACTC
85021	TAAAATTTAC	AACTGACCGT	GATGCGCATT	TTTTCTAGAC	AAACCTAAAG	GTAAATCTGC
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85141	CATTTTCATC	AAAGTCTACA	TGGGTCTATC	CCAAGTCACC	AGAAGAGCCA	GGGGAAAAGG
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85681	ATCTAACTTT	TGAAGTCTCA	GAGGTTTTAC	ACTTTCCATA	ACAAATAGTT	AAGAACCCCC
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85861	CAGAGACAGC	GATCAGGTGG	GTAGCCTAGT	TAGGATTTTA	ACCCTTCGGT	TTCCAACAAA
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86221	GAAAGAGCTG	GGTGGGCACG	CGGCATCGCC	ATGGGCGGAG	TGGCCCAGGT	GCGCTGGCTG
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Homo sapiens transforming growth factor, beta receptor II (70/80kDa),
antisense sequence

Derived from BC040499

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LOCUS AY497473

DEFINITION Homo sapiens transforming growth factor, beta receptor I
(activin A receptor type II-like kinase, 53kDa) (TGFBRI) gene

coding sequence in reverse complement

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1441 CGCCGCCGCC GCCCGCCCG CCAGCACGAG GAGGAGCAGC CGGGGACGCG GAGCAGCGAC
1501 CGCCGCCTCC AT

SEQ ID NO: 95

LOCUS AY497473

DEFINITION Homo sapiens transforming growth factor, beta receptor 1
(activin A receptor type II-like kinase, 53kDa) (TGFBRI) gene

mRNA in reverse complement

1 AAACACTATA GGTTTAAACA TAGAGACTTT CAGCAATTCT ACTCATTTCC ATTAGAAAGA
61 CACAGAAGTG GCACTTACTG GTATAGTACA ATCCCATTTT GAAGGCATGT AATGTTCTGA
121 ATAAGTGAAA GAACAATAAT AGTATACAAA ATACAATTGC ATGAATTATG TTCCTCACTA
181 CTATATGAGG TCATTTTATG ACTCAAGATA AGAGTTTAT AAGTGTTAGT TTTAAGATCC
241 TGAAAAACTA TAGAACAGTA CATTCAAAGT CTGAATCAAG GAAACTCTAG TGGTTCAGAA
301 TCCTCTGAGA ATGTACTAAC CAGGAGTAAA TCACTTTCTT TAGTAATAAG ACATGTTTCA
361 TTGTAATTCA GCAATCCAAC TCCTTTGCCC TTAAAGATGA TCTCCAGCAC AGCAGAGTTA
421 CCTAAAGTTA AGACCAGCAA TCATCTTTT AAAAACAAG TTTTGTTAAT AAAAAATAAA
481 GGTAGACTAC ACATTTTCTG TCCTGGGAAA GAAGCGTTCA TAGTGCACAG AAAGGACCCA
541 CATGGCTGTT TCCTGGGTCC AAAGAAATCC TGGGAAGTTT TTAATTGACT TTATTACACT
601 GCTGCAAAAG GAAGCAATAT CCTTCTGTTC CCTCTCAGTG AGGTAGAACA ATTGACCTCC
661 CAAATTAATA CCCAGGAGCA GATCTGAAGA AAAAAGGAGA GTTCAGGCAA AGCTGTAGAA
721 TTACATTTTG ATGCCTTCCT GTTGACTGAG TTGCGATAAT GTTTTCTTAA TCCGCAATGC
781 TGTAAGCCTA GCTGCTCCAT TGGCATACCA ACATTCTCTC ATAATTTTAG CCATTACTCT
841 CAAGGCTTCA CAGCTCTGCC ATCTGTTTGG GATATTTGGC CTTAACTTCT GTTCACAAAC
901 AACTTTTCTC ATTTCTTCAA CTGATGGGTC AGAAGGTACA AGATCATAAT AAGGCAGTTG
961 GTAATCTTCA TGAATTCCAC CAATGGAACA TCGTCGAGCA ATTTCCCAGA ATACTAAGCC
1021 CATTGCATAG ATGTCAGCAC GTTTGAAGGA TTCAAAATGT TTCATATTTA TGGAATCATC
1081 GAGAACTTCA GGGGCCATGT ACCTTTTGTG TCCCACTCTG TGGTTTGGAG CAATATCAAT
1141 GGTATCTGTG GCTGAATCAT GTCTTACTGC CAGTCCTAAG TCTGCAATAC AGCAAGTTCC
1201 ATTCTTCTTT ACCAAGATAT TCTTTGATTT CAAATCTCTA TGAGCAATGG CTGGCTTTCC
1261 TTGGGTACCA ACAATCTCCA TGTGAAGATG GGCAAGACCG CTCGCCGTGG ACAGAGCAAG
1321 TTTTATCATT CCTTCCACAG TAACTGTGTA TCTGTTTAAG TAATCAAAAA GGGATCCATG
1381 CTCATGATAA TCTGACACCA ACCAGAGCTG AGTCCAAGTA CCATTGTCTT TATTGTCTGC
1441 TGCTATAAAT CCCAGGATGT TTTTATGACG TAACATTACA GTTTGATAAA TCTCTGCCTC
1501 ACGGAACCAC GAACGTTCCT CTCTAGAGGA GAATATCTTA ACAGCAACTT CTTCTCCCCG
1561 CCACTTTCCT CTCCAAACTT CTCCAAATCG ACCTTTGCCA ATGCTTTCTT GTAACACAAT
1621 AGTTCTCGCA ATTGTTCTCT GAACAAGCAA TGGTAAACCT GAGCCAGAAC CTGACGTTGT
1681 CATATCATAA ATTAAGTCTT TCAACGTAGT ACCCTCTGAA ATAAAAGGGC GATCTAATGA
1741 AGGGTCCTCT TCATTTGGCA CTCGATGGTG AATGACAGTG CGGTTGTGGC AGATATAGAC
1801 CATCAACATG AGTGAGATGC AGACGAAGCA CACTGGTCCA GCAATGACAG CTGCCAGTTC
1861 CACAGGACCA AGGCCAGGTG ATGACTTTAC AGTAGTTGGA AGTTCTATTT TATTGCAATG
1921 GTCCTGATTG CAGCAATATG TTGTAGTCAC AGACCCAGTT TTTGAAGAGG GTGCACATAC

1981 AAACGGCCTA TCTCGAGGAA TTAAGTCAAT TTCAGCTATA CACATGCTGT TGTGTATAAC
2041 TTTGTCTGTG GTCTCTGTGA CAGAGACAAA GCAGAGCCCA TCTGTCACAC AAGTAAAATT
2101 GTCTTTTGTA CAGAGGTGGC AGAAACACTG TAACGCCGTC GCCCCGGGA GCAGCGCCGC
2161 CGCCGCCGCC GCCGCCGCC CCAGCACGAG GAGGAGCAGC CGGGGACGCG GAGCAGCGAC
2221 CGCCGCCTCC ATGGTCCCGC CGCCACCGCC TGTGGCCCGG CCCGGCCCGG CCGCGCCGCT
2281 GCCTCACCCC AGCAAACCTC GCCTCGCC

SEQ ID NO: 96

LOCUS AY497473

DEFINITION Homo sapiens transforming growth factor, beta receptor I
(activin A receptor type II-like kinase, 53kDa) (TGFBRI) gene

gene in reverse complement

1 CCTAGGATGG GCAGTATAAA CAACTGTGTT TTAAATGAC AAAATTATTA CTCTAATCAA
61 ATTTATCTGC AGTTATCGAC AGTAATCATG ATCCATCCCA CCTTTAAGT TTCTTTCATT
121 TTCAATATCA GCCAATTGTG GTTTATCAAA CCATCCCTAG CCAAAAAAGG AATTAACTCG
181 AGTAATACGT AAAGTCAATT TAGAACTAAA CTCCAACTTT AAAAAAATTC CCTGATTAT
241 CAAAAGTACA TTTTATCCAC TTAGGTAAGA AAAGTATAAT TGTAAC TCA TCTTTGATTC
301 AATAAAAAAT ATCTTCAGCA AAAGTGGATA ACCTTACATG AAAGTGAGAA ATCATGTATT
361 ACAACTTTAA ATCAGACAAC TTTTGGTATA TTCTTAAAT TATATAAAAA TAGTTTTAGT
421 GATAAAATGC ATTGGTCCCC TGGATTTTCAT AAAGCAGATC TGGTAGGCTT AGAAATGGCC
481 CAAAAACAAC AACAAAAAAA AAAAAACAAA AAAAAACCC CCACAAAAAA AGTACCTGAT
541 CACAGAATTA GAGATTATTA TTAAACAAGT AATACAACAC AACTATAAAA ACAACCTCT
601 CAACTCATT CATTTGCTTC AATGAAATTA TGGTAACTAC AGAAAAAAC TCAACTTTGT
661 AGTCAAAATA GTAACCTCTA AGCATTTTTTC CCATGATGTT TTAAACACA TGAAATTGAC
721 ACTAAATTCC TATGTAATAT GTCACCTATT CTAAAATTAC TTTGGTTTTA AGATCAAATA
781 GTCTTTCAAA TTTATTCTAC GTATAAGAGA TAAGACATTA TCAGAATGCA ACTCATTCAG
841 TGTAAATGGC CACTTTCTCT TCCTGACCAA AATACTGTAT GGGTACTCT GACCCTGTAT
901 CGGGGAAC TGATAGCTAT AAAGTCGAAG TCTGCTCTCA GAGCTATGAT AGTTTTTTCT
961 CCCCTCAGAA TAAGATCACA GTGATAAAAG GACTTCGAAA ACTGTAAAAG CCCTGCAGAG
1021 ACTTCATAGC ATTGGAAGTA AAAACCAGTT ATTATAAGCT AGTTTCAACT TAATGTAAGA
1081 AGACCATGAC AAGTTTGCTT TCAATATTTG ACCAAAGACA TCTGTAAATG GAGAAAAACC
1141 TATACTCAGA ATGTTCTTTA GCTACCACCT CTCCAAGTA ACAAGGGTGC ACTGAATGCA
1201 TTACATAAAT TACATGTAAG CAGTTGCAAT GTACGCACAC ATAAGGAAAC ACTGAATTAA
1261 AAGCTGCCTT CCTCAAAGTG TAGTGAGACC TCAAAACCAC ACTAGCTCTA ACCTCAGTTA
1321 CAAAGACAGA GGATCCACCG AACGTTTACT CCTACATACA TAACAAATGT GACTTTCTTG
1381 CACATCTGTT ATCTATTCAA ATTATTAAC ACCTTCGCCT TCCTAGAAAA AGGCCTATTA
1441 TTTAATATTA ACCATATTCT AATTTTAAAT GTAATTCATG TCTTAAAAAA TAAGTCTTTG
1501 AACAGATAAA GAAAAAATG GCTTACAGAA TACCACATAA CTTTTCACAA GCAGCTAGAC
1561 AGACTTTCCC TTTTAGAAAA ATTAGTCTGT ATGCTACAAA TATTAAAGTA CTATAAGCAT
1621 CTAGAGTGCC ACTTGATTTT TAAAAAGTAT ACTTAGACAA CACAATTAAA ATGCAAAAGC
1681 TTGATGTGAG AATATTCAAA CATGACCATG CTAATAATTT ACTAATTAAT GCCACTTCAT

1741 TTCTTTAGTG GCTTAAGCAC ATTTTGGTAG GAGAAAGGCA TTTTCAGAAT AGAATACCAA
1801 ATGACATACC ACAAAAACCC TTCCAAAAC AAAACAGAAA AAGTTTGGGT TACCCAGATA
1861 AATAAGCTTT TTGAATTCAA ACACTATAGG TTTTAACATA GAGACTTTCA GCAATTCTAC
1921 TCATTTCCAT TAGAAAGACA CAGAAGTGGC ACTTACTGGT ATAGTACAAT CCCATTTTGA
1981 AGGCATGTAA TGTTCTGAAT AAGTGAAAGA ACAATAATAG TATACAAAAT ACAATTGCAT
2041 GAATTATGTT CCTCACTACT ATATGAGGTC ATTTTtagac TCAAGATAAG AGTTTTATAA
2101 GTGTTAGTTT TAAGATCCTG AAAAActata GAACAGTACA TTCAAAGTCT GAATCAAGGA
2161 AACTCTAGTG GTTCAGAATC CTCtgagaat GTACTAACCA GGAGTAAATC ACTTCTTTA
2221 GTAATAAGAC ATGTTTCATT GTAATTCAGC AATCCAActC CTTTGCCCTT AAAGATGATC
2281 TCCAGCACAG CAGAGTTACC TAAAGTTAAG ACCAGCAATC ATCTTTTAA AAAACAAGTT
2341 TTGTTAATAA AAAATAAAGG TAGACTACAC ATTTTCTGTG CTGGGAAAGA AGCGTTCATA
2401 GTGCACAGAA AGGACCCACA TGGCTGTTTC CTGGGTCCAA AGAAATCCTG GGAAGTTTTT
2461 AATTGACTTT ATTACACTGC TGCAAAAGGA AGCAATATCC TTCTGTTCCC TCTCAGTGAG
2521 GTAGAACAAT TGACCTCCCA AATTAAAACC CAGGAGCAGA TCTGAAGAAA AAAGGAGAGT
2581 TCAGGCAAAG CTGTAGAATT ACATTTTGAT GCCTTCCTGT TGA CTGAGTGT GCGATAATGT
2641 TTTCTTAATC CGCAATGCTG TAAGCCTAGC TGCTCCATTG GCATACCAAC ATTCTCTCAT
2701 AATTTTAGCC ATTACTCTCA AGGCCTACAA GAAAATATAA AAAAAAAAAAT TAATGCATGC
2761 ACCATTTTCC ATTGGTCTGG ATAAGAATTT TTACGTGTAA ATTTTCTTTT TAAATGACAT
2821 ATACACTTGT TATTGTTTAA GCATTATTTG TAATAGCAA TGAGTAGAAA TTACATAAAT
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2941 TAGCAAACCT GAAAAGGCCG AATCCTAAAC CAGAGCTGGG CAAAGCAAAG AAGAAATCTG
3001 ACCTCACACT GAAATTTTAA GTTTGTACTT TGAAGTATTC ACATCAAAT TTTCTTTCTT
3061 TTTTTTTTTT TTGAGACAGG GTCTCACTCT GCCGCCCAA GTGGAATGCA ATGGCATGCC
3121 CTCAGCTCAC TGCAGCCTTG ACCTCCCAGG CTCCAGCAAT CCTCCCActT CAGCCTCCCA
3181 AGTAGATCAA ATTTCTAAAA GACAAAATCT AGCAGCACTC TCATTTATTA AACTATGTCA
3241 CATGCAAATT CCTTAAGCAT GCTGAAATAC ATTTTATTTA TTTGGGCCTG GAGATGTGAT
3301 TTTGTTGGAG GTAGCAAGCT CTCTTGCTTA TCAGAGGTTT TGCTGAGTCC TACAATAGTT
3361 TAAGACGTAA AATCAACTAC TGAActGAAC AGCTTTTAT AGCCTTTTTA AGCTACAAAT
3421 CTTCAAACCT GGAGGAATAT GCTCTGCTTC ACCAATATTG TAATAGTAAC AGCTAGCAAT
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3961 AATATGAAAA CCAAATTATT CTGTTTTTAA ACATTGGTTT GACTGCTATG AAAAAGAAAA
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4081 AGTTTtagAAA ATTGCCTAAT ATCAAAAAGA AATACTCACT TCACAGCTCT GCCATCTGTT
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4201 GTCAGAAGGT ACAAGATCAT AATAAGGCAG TTGGTAATCT TCATGAATTC CTGTATCAGT
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4321 CTGAGAGACC TATTACAGTG TTTCACTACT AAAGTAGGTA TGTGGAACAG AGATTACAGC

4381 TTTCTCTATC TCATCCACAT CTGTATCCAC AAGCCACTTC CCTGAGTTGA TATTCCACCC
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4981 GCTTCCTAGG TGAGCCTCTC AAGCAGCTGT CCATTCTAAA GAACTATATT CCAATATAAC
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5161 GTTTTCTCTG GCACTCGGTG ACATCCTGTT TCAGATAATG GACTGTACAT AATTTCAATC
5221 AATTAAAAA AGAAGACAAT TCTTGAACAA CTTCTGCTCA TGACAAACTA CTGGGGGAGA
5281 GGAGAGCAAT TTACCACCAA TGGAACATCG TCGAGCAATT TCCCAGAATA CTAAGCCCAT
5341 TGCATAGATG TCAGCACGTT TGAAGGATTC AAAATGTTTC ATATTTATGG AATCATCGAG
5401 AACTTCAGGG GCCATGTACC TAAAAAAAT TTGCAAAAAG AACTTTGAAA ATCATCCCCT
5461 TACTGCCATA TTTGGATGAA CCTCCTTTCA GACATTTCTT TATACATAGA CATATGTACA
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5581 CATTAATGAT GTCAACTAAA TCCCACAAAA TGCTAAAATA GCAGTTTCAC ACTATCTGCC
5641 TCATGATCTT GGTTTCCAAT GAAAGACATA CATAACAATT GTGACTGTTA AAGGTGTCCT
5701 AATGTACACC ACCTATACAC GTACTAGGTA GAAACCATGC ATTTTAATTT AGAAGTCTTC
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6961 GAAGGGAAAA AAGGTGATTT CAGAAGATAT TAAATATAGT TGTTCAAAAAG TATACCTTTT

7021 TGTTCCTACT CTGTGGTTTG GAGCAATATC AATGGTATCT GTGGCTGAAT CATGTCTTAC
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7201 CTTAAAAGGT AATACCAATC ACAACTCACA TCTTTAGGTT CAAAAGTCTC TTCTCCCAAC
7261 CCAAATTATC AAAGCATTTT AGCCACATG ACCTACAATA CTTACGGGCA TTATTAAACT
7321 CAAGTGAATC ACTACACCAA AAGTCACTGA ATTTATATTT CTTTAAAGAA AATGTGGACA
7381 ATAACATGCT TTAAAAGATG AACAACCTCA AGACTGGGGC AAAAAAAG TTATCAGTTT
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7501 GCCCAGGAAC CAAGCATGTA GAACATCACT TCCCTATCAA CTGCAATGTA CTCAGTATTA
7561 AGTATATTAT CTTTGATGCT AACCCTAGA AAATGTTATT AAAAAATAAT AATTATAATG
7621 TGGAAAACCT GGAACCTTCA TACACTGCTG GCAGGAATGT AAAATGGTTC AGGCACTTTA
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8281 AATAACTACA AAGATGGAGC TAAGATGTGA ACTAGCACTT ATGCTGTATG TAAAGTGGGG
8341 AGTGGGGGAG CCATTGGGTT GCAAGTGGAC AACTGCTAGA GCAGAGAGAT ATACTGGCAT
8401 CTGAAATCCC ACATGCACAA AAACCTACAGC ATACAAATGT CATAACTAAA ACTTAGTATT
8461 TAATTTTTCA ACTGTAAAC TATCTCATGC AGTCTCCTTA TCTCAAGGTC AAATATAATT
8521 ATTAGATGGC CAGATAACAG TTACCTAGCA TGTTGATGTT TACAAAGCAC TTTCACATTT
8581 CATTGATAC TACACATAAA AATATATTCA GTTGGACCTG AATTCTGAAA CTGAGATCCT
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8701 AACGACTAGA GAATCTCTAA ACAAATTTCC AGATTCTAG CTCTACCTGA AATTTTGAAC
8761 TGAAAGATAA AATGTTCTCA TCTAAAAAAT TTGTTTTTAA TATCTCCAGT TAGGCCACCT
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8941 TACCTCAGCC CCCTGAGTAG CTGGGACTAC AGGTGCATGC CACCATGCCC GACTAATTTT
9001 TTGTATGTTG GTAGAGATGC GGTTTTGTCA TGTGCCCCAG GCTGGCCATG AACTCCTGAG
9061 ATCGGGCGAT CTGCCCACCT CAGCCTCCCA AAGTGCTGGG ATTATAGGCA TGAGCCACCA
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9241 CCGCTCGCCG TGGACAGAGC AAGTTTTATC ATTCCTTCCA CAGTAACTGT GTATCTGTTT
9301 AAGTAATCAA AAAGGGATCC ATGCTCATGA TAATCTGACA CCAACCAGAG CTGAGTCCAA
9361 GTACCATTGT CTGTAAAACA GAATTAACAT TTCGGTTGGG CTGCAGACCA TTTATGATTT
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9481 CCACCTTAAG TCTGTATTTT CTTACATTT TCTTCTACAT TGTTTGTGTTT ATACTTTTAT
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9781 GAAGTCTCCG GAGACCAGTG TGGCCACAGT GGAATGGAA GAGTATGGGA CAAAACCTGAA
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9961 ACCTCTAACA CATGGGGAAG CTGAAATAGG AACTGAAATG TCAGGAGCAA AACTGGAAAA
10021 GCTGGGACTA AACTCAAACA ACGAGGAACG TGGGTTCCAA AATTCCTCT GTAAGCCAAA
10081 ACACGAGTTT AAAACATGTT TTCTCATAGG AATAATGGTA AAGACACTAG CTAGGCTCCT
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10441 TGCTGGTTGT AAACCAAAG AAAAAATCCA TATTGACATG AAACAGCTTC TATTTTGAAG
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10981 TAGTTCCTCAT GGTGACCACC AGATGACAGC ATCAGCCTGG TTAGAAGTTC AGGGCACAGA
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11161 CATGAATGTG GCTATGTTCT TAAGGAAGAA ATTACCACTT ATAAAATCAG TACCTTCATA
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11281 AACAAGGAAA GTCTAGGGTC ATCAAACACA GTAAATAAAG AAAAGTTGT TTTAAGAGTT
11341 GGGGGAGGAA ATAAATGGTG ATAAAGGCAG AAACGAAAAT GAGAACTAAG GATTTGGTCA
11401 GACTGATTAC TATTTTTTGT TTGTTTTTGT TTTGTTGTTG TTTTTTTTTT GAGACAGAGT
11461 CTCCCTGTGT CGCCCAGGCT GGAGTGCAGT GGTGCGATCT CAGCTCTGAC TGCAACCTCC
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11941 TACCAGTTTT CAGAAAAGAT AGAAGAACAA GTTAAGAGAC ACTATGGAAA TGCAATCAGC
12001 AAAATCCAGA ATGTGATAGG CCCTTCAGGA TAAACAATCC AATTTCTTCA ACAAATAAGC
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12181 AGACAATTAT AGAATTGAAC CTAACCTGGAT ATTTGATAAC ATTTAAAAAA CTGACAATGG
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41641 CTGTGTGTAT ACTTTGCAAG TCAATTTTTT TTAAGTTAGA TTAGAAATTG TTCTTTGAGG
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41761 TTAGTCCACT AGTATTTAAG AAAGTGATGT CTGAGATGAA TAATTACAAG TCTACCAACC
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42181 TTCAGAGAAC TCTGTGTTAC GTAAGCCATG ACCAAGGAAG AACTGCAAAA GGCAAGAGGT
42241 GTGTCGACAT TTGCAAGGGG CTCTGTGGTT TGAAGAGACA CGTTCTCACA TCAGAAGGGC
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43321 AAGTCAGTGT AAGTCTAAA GTGTCCAAGA AGCCTCCCC AATCATTTCA GCTTACACTA
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